

SEQUENCE LISTING

<110> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL

<120> NOVEL INHIBITORS OF NF-kappaB ACTIVATION

<130> 2676-4554US

<140> 09/702,953

<141> 2000-10-31

<150> PCT/BE99/00055

<151> 1999-05-05

<150> US 09/702,953

<151> 2000-10-31

<150> 98201472.2

<151> 1998-05-06

<160> 19

<170> PatentIn version 3.2

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Arg Leu Lys Gly Lys Met Gln Gly Ile Lys Met Leu Gly Glu Leu Leu	
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Gln Val His Pro Ala Thr Ser Thr Ala Ala Thr Thr Thr Ala Thr Ala	
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Lys Val His Lys Asn Glu Gln Arg Thr Ser Ile Leu Gln Thr Leu Cys	
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Glu Gln Leu Arg Gln Glu Asn Glu Ala Leu Lys Ala Lys Leu Asp Lys	
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Thr Glu Leu Lys Lys Leu Leu Met Asn Ser Ser Cys Lys Glu Gly Leu	
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Cys Gly Gln Pro Ser Ser Pro Lys Pro Glu Gly Ala Gly Lys Lys Gly	
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Val Ala Gly Gln Gln Gln Ala Ser Val Met Ala Ser Lys Val Pro Glu	
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Lys Glu Leu Arg Gln Lys Val Arg Tyr Leu Gln Asp Gln Leu Ser Pro	
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Leu Thr Arg Gln Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu Asn	
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Phe Glu Glu Asp Phe Gln Arg Glu Arg Ser Asp Arg Glu Arg Met Asn	
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His Pro Pro Pro His Pro Asn Ser Arg Leu Phe His Leu Pro Glu Tyr	
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acc tgg cgt cca ccc tgt gca ggg att cgg aat cag agc tct caa gtg	1991
Thr Trp Arg Pro Pro Cys Ala Gly Ile Arg Asn Gln Ser Ser Gln Val	
610 615 620 625	

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Asp Cys Asp Gly Pro Gln	
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35 40 45

Leu Glu Glu Ser Gln Met Glu Ala Ser Arg Leu Arg Gln Lys Ala Glu
50 55 60

Glu Leu Val Lys Asp Ser Glu Leu Ser Pro Pro Thr Ser Ala Pro Ser
65 70 75 80

Leu Val Ser Phe Asp Asp Leu Ala Glu Leu Thr Gly Gln Asp Thr Lys
85 90 95

Val Gln Val His Pro Ala Thr Ser Thr Ala Ala Thr Thr Thr Ala Thr
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Ala Thr Thr Gly Asn Ser Met Glu Lys Pro Glu Pro Ala Ser Lys Ser
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Gln Asn Ser Pro Glu Thr Gly Ser His Pro Thr Asn Met Met Asp Leu

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Leu	Phe	Thr	His	Leu	Gly	Arg	Met	Ala	Leu	Glu	Phe	Asn	Arg	Leu	Ala
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Leu	Cys	Gly	Gln	Pro	Ser	Ser	Pro	Lys	Pro	Glu	Gly	Ala	Gly	Lys	Lys
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Gly	Val	Ala	Gly	Gln	Gln	Gln	Ala	Ser	Val	Met	Ala	Ser	Lys	Val	Pro
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Gln Lys Leu Val Asp Leu Gln Lys Gln Val Thr Glu Leu Glu Ala Glu			
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Arg Glu Gln Lys Gln Arg Asp Phe Asp Arg Lys Leu Leu Leu Ala Lys			
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Ser Lys Ile Glu Met Glu Glu Thr Asp Lys Glu Gln Leu Thr Ala Glu			
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Ala Lys Glu Leu Arg Gln Lys Val Arg Tyr Leu Gln Asp Gln Leu Ser			
405	410	415	
Pro Leu Thr Arg Gln Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu			
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Asn Lys Ala Leu Glu Glu Ala Leu Ser Ile Gln Ala Ser Pro Ser Ser			
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Pro Pro Ala Ala Phe Gly Ser Pro Glu Gly Val Gly Gly His Leu Arg			
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Lys Gln Glu Leu Val Thr Gln Asn Glu Leu Leu Lys Gln Gln Val Lys			

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Gln Val Thr Leu Thr Asn Ala Gln Leu Lys Thr Leu Lys Glu Glu Glu						
	515		520		525	
Lys Ala Lys Glu Ala Leu Lys Gln Gln Lys Arg Lys Ala Lys Ala Ser						
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Gly Glu Arg Tyr His Met Glu Pro His Pro Glu His Val Cys Gly Ala						
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Tyr Pro Tyr Ala Tyr Pro Pro Met Pro Ala Met Val Pro His His Ala						
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Tyr Lys Asp Trp Ser Gln Ile Arg Tyr Pro Pro Pro Pro Val Pro Met						
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Glu His Pro Pro Pro His Pro Asn Ser Arg Leu Phe His Leu Pro Glu						
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Tyr Thr Trp Arg Pro Pro Cys Ala Gly Ile Arg Asn Gln Ser Ser Gln						
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35 40 45

Asp Ser Glu Leu Ser Pro Pro Thr Ser Ala Pro Ser Leu Val Ser Phe
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Asp Asp Leu Ala Glu Leu Thr Gly Gln Asp Thr Lys Val Gln Val His
65 70 75 80

Pro Ala Thr Ser Thr Ala Ala Thr Thr Thr Ala Thr Ala Thr Thr Gly
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Asn Ser Met Glu Lys Pro Glu Pro Ala Ser Lys Ser Pro Ser Asn Gly
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Gln Gln Gln Ala Ser Val Met Ala Ser Lys Val Pro Glu Ala Gly Ala
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Lys Gln Gln Tyr Glu Gln Lys Ile Thr Glu Leu Arg Gln Lys Leu Val
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Asp Leu Gln Lys Gln Val Thr Glu Leu Glu Ala Glu Arg Glu Gln Lys
340 345 350

Gln Arg Asp Phe Asp Arg Lys Leu Leu Leu Ala Lys Ser Lys Ile Glu
355 360 365

Met Glu Glu Thr Asp Lys Glu Gln Leu Thr Ala Glu Ala Lys Glu Leu
370 375 380

Arg Gln Lys Val Arg Tyr Leu Gln Asp Gln Leu Ser Pro Leu Thr Arg
385 390 395 400

Gln Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu Asn Lys Ala Leu
405 410 415

Glu Glu Ala Leu Ser Ile Gln Ala Ser Pro Ser Ser Pro Pro Ala Ala
420 425 430

Phe Gly Ser Pro Glu Gly Val Gly Gly His Leu Arg Lys Gln Glu Leu
435 440 445

Val Thr Gln Asn Glu Leu Leu Lys Gln Gln Val Lys Ile Phe Glu Glu
450 455 460

Asp Phe Gln Arg Glu Arg Ser Asp Arg Glu Arg Met Asn Glu Glu Lys
465 470 475 480

Glu Glu Leu Lys Lys Gln Val Glu Lys Leu Gln Ala Gln Val Thr Leu
485 490 495

Thr Asn Ala Gln Leu Lys Thr Leu Lys Glu Glu Glu Lys Ala Lys Glu
500 505 510

Ala Leu Lys Gln Gln Lys Arg Lys Ala Lys Ala Ser Gly Glu Arg Tyr
515 520 525

His Met Glu Pro His Pro Glu His Val Cys Gly Ala Tyr Pro Tyr Ala
530 535 540

Tyr Pro Pro Met Pro Ala Met Val Pro His His Ala Tyr Lys Asp Trp
545 550 555 560

Ser Gln Ile Arg Tyr Pro Pro Pro Pro Val Pro Met Glu His Pro Pro
565 570 575

Pro His Pro Asn Ser Arg Leu Phe His Leu Pro Glu Tyr Thr Trp Arg
580 585 590

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Gly Pro Gln
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Pro Glu Pro Ala Ser Lys Ser Pro Ser Asn Gly Ala Ser Ser Asp Phe
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Glu Val Val Pro Thr Glu Glu Gln Asn Ser Pro Glu Thr Gly Ser His
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Pro Thr Asn Met Met Asp Leu Gly Pro Pro Pro Pro Glu Asp Ser Asn
85 90 95

Leu Lys Leu His Leu Gln Arg Leu Glu Thr Thr Leu Ser Val Cys Ala
100 105 110

Glu Glu Pro Asp His Ser Gln Leu Phe Thr His Leu Gly Arg Met Ala
115 120 125

Leu Glu Phe Asn Arg Leu Ala Ser Lys Val His Lys Asn Glu Gln Arg
130 135 140

Thr Ser Ile Leu Gln Thr Leu Cys Glu Gln Leu Arg Gln Glu Asn Glu
145 150 155 160

Ala Leu Lys Ala Lys Leu Asp Lys Gly Leu Glu Gln Arg Asp Leu Ala
165 170 175

Ala Glu Arg Leu Arg Glu Glu Asn Thr Glu Leu Lys Lys Leu Leu Met
180 185 190

Asn Ser Ser Cys Lys Glu Gly Leu Cys Gly Gln Pro Ser Ser Pro Lys
195 200 205

Pro Glu Gly Ala Gly Lys Lys Gly Val Ala Gly Gln Gln Gln Ala Ser
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Val Met Ala Ser Lys Val Pro Glu Ala Gly Ala Phe Gly Ala Ala Glu
225 230 235 240

Lys Lys Val Lys Leu Leu Glu Gln Gln Arg Met Glu Leu Leu Glu Val
245 250 255

Asn Lys Gln Trp Asp Gln His Phe Arg Ser Met Lys Gln Gln Tyr Glu
260 265 270

Gln Lys Ile Thr Glu Leu Arg Gln Lys Leu Val Asp Leu Gln Lys Gln
275 280 285

Val Thr Glu Leu Glu Ala Glu Arg Glu Gln Lys Gln Arg Asp Phe Asp
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Arg Lys Leu Leu Leu Ala Lys Ser Lys Ile Glu Met Glu Glu Thr Asp
305 310 315 320

Lys Glu Gln Leu Thr Ala Glu Ala Lys Glu Leu Arg Gln Lys Val Arg
325 330 335

Tyr Leu Gln Asp Gln Leu Ser Pro Leu Thr Arg Gln Arg Glu Tyr Gln
340 345 350

Glu Lys Glu Ile Gln Arg Leu Asn Lys Ala Leu Glu Glu Ala Leu Ser
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Ile Gln Ala Ser Pro Ser Ser Pro Pro Ala Ala Phe Gly Ser Pro Glu
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Arg Ser Asp Arg Glu Arg Met Asn Glu Glu Lys Glu Glu Leu Lys Lys
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Gln Val Glu Lys Leu Gln Ala Gln Val Thr Leu Thr Asn Ala Gln Leu
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Lys Thr Leu Lys Glu Glu Glu Lys Ala Lys Glu Ala Leu Lys Gln Gln
450 455 460

Lys Arg Lys Ala Lys Ala Ser Gly Glu Arg Tyr His Met Glu Pro His
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515 520 525

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Gln Asp Gly Ala Pro Arg Ala Ala Ala Ala Leu Cys Gly Leu Tyr His
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Glu Ala Gly Gln Gln Leu Gln Arg Leu Lys Asp Gln Leu Ala Ala Arg
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gac gcc ctc atc gcg agc ctc cgc acc cgc ctc gcg gct ctg gaa ggg 256
Asp Ala Leu Ile Ala Ser Leu Arg Thr Arg Leu Ala Ala Leu Glu Gly
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cac acg gcg ccg tca ctc gtg gac gca ctt ctg gat cag gtg gag cgc 304
His Thr Ala Pro Ser Leu Val Asp Ala Leu Leu Asp Gln Val Glu Arg
60 65 70

ttc cgt gag cag ctg cga cga cag gag gaa ggc gct tcg gag acc cag 352
Phe Arg Glu Gln Leu Arg Arg Gln Glu Glu Gly Ala Ser Glu Thr Gln

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	125	130	135	
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Ala Ala Ser Asp Val Leu Cys Arg Ser Leu Ala Asp Glu Thr His Gln				
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Leu Arg Arg Thr Leu Ala Ala Thr Ala His Met Cys Gln His Leu Ala				
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aaa tgt ctg gat gaa cga cag tgt gca cag gga gac gct ggg gag aaa				640
Lys Cys Leu Asp Glu Arg Gln Cys Ala Gln Gly Asp Ala Gly Glu Lys				
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agc cct gct gag cta gag caa aca agc agc gat gct tct ggc cag agt				688
Ser Pro Ala Glu Leu Glu Gln Thr Ser Ser Asp Ala Ser Gly Gln Ser				
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gtt att aag aag tta cag gaa gaa aat cga ctg tta aaa cag aag gtg				736
Val Ile Lys Lys Leu Gln Glu Glu Asn Arg Leu Leu Lys Gln Lys Val				
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Thr His Val Glu Asp Leu Asn Ala Lys Trp Gln Arg Tyr Asp Ala Ser				
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Arg Asp Glu Tyr Val Lys Gly Leu His Ala Gln Leu Lys Arg Arg Gln				

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Val Pro Leu Glu Pro Glu Leu Met Lys Lys Glu Ile Ser Arg Leu Asn				
	255	260	265	
aga cag ttg gag gag aaa ata agt gac tgt gcg gaa gca aac cag gag				928
Arg Gln Leu Glu Glu Lys Ile Ser Asp Cys Ala Glu Ala Asn Gln Glu				
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ctg aca gcc atg agg atg tcc cgg gac act gcg ctg gag cga gtg cag				976
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	315	320	325	330
aag atc atg tcc ttg atg tac caa gtg tcc cag aga cag gac tcc cgg				1120
Lys Ile Met Ser Leu Met Tyr Gln Val Ser Gln Arg Gln Asp Ser Arg				
	335	340	345	
gag cca gga ccc tgt cgg att cat acg ggg aac aaa act gcc aag tac				1168
Glu Pro Gly Pro Cys Arg Ile His Thr Gly Asn Lys Thr Ala Lys Tyr				
	350	355	360	
tta gag atg gat gca ctg gag cat gtg acc cct ggc ggc tgg agg cct				1216
Leu Glu Met Asp Ala Leu Glu His Val Thr Pro Gly Gly Trp Arg Pro				
	365	370	375	
gag tct agg tcc caa cag atg gaa cct tct gca gag ggt ggg cat gtg				1264
Glu Ser Arg Ser Gln Gln Met Glu Pro Ser Ala Glu Gly Gly His Val				
	380	385	390	
tgc aca gcc cag aga ggt cag ggt gac ctt cag tgc cct cat tgc ctg				1312
Cys Thr Ala Gln Arg Gly Gln Gly Asp Leu Gln Cys Pro His Cys Leu				

395	400	405	410	
cgg tgc ttc agt gat gag caa ggc gag gca ttc ctc agg cac ctg tct				1360
Arg Cys Phe Ser Asp Glu Gln Gly Glu Ala Phe Leu Arg His Leu Ser				
	415	420	425	
gag tgc tgc caa tga gccagacatt gcccgtgtga cccatgacca ccatagctgc				1415
Glu Cys Cys Gln				
	430			
tctaaggac tgggaggggt cctcagactc agttttcaac tcagtgtgtt gcattctcct				1475
gggatctagg gcccaaatgg gcagggtcac tggaaggcca tcttggtttc atttgaccat				1535
ggtgagactt ggtcagaggg aactattgac agagcaggag gaagaggggtg gggtcaggga				1595
catcaagtgg acatcagttt tgtctcacgt agagtttga gtgagctgtc aattcaaagc				1655
tgcaagctat cagttgtggg aatattctga agcctgcttg cacctagagt tatgccactt				1715
gctggaaggg gaagttgctg tgggagcagt gtgtcctctt tctaggggtg tagctccatc				1775
ctgttgagta gtgagataca ctccctgact ggtctgtgct gcattacagt tacatgatac				1835
actagaacct tcccaaactc agcagagcca cacagctgca tccagtacca tcaccctgca				1895
aaacacttgt atttccaaaa gggaaagcac ctttatttcc taatcattta tttttataat				1955
aaatggcttt ac				1967

<210> 6

<211> 430

<212> PRT

<213> Mus musculus

<400> 6

Met	Ser	Ser	Gly	Asp	Pro	Arg	Ser	Gly	Arg	Gln	Asp	Gly	Ala	Pro	Arg
1			5					10					15		

Ala Ala Ala Ala Leu Cys Gly Leu Tyr His Glu Ala Gly Gln Gln Leu
20 25 30

Gln Arg Leu Lys Asp Gln Leu Ala Ala Arg Asp Ala Leu Ile Ala Ser
35 40 45

Leu Arg Thr Arg Leu Ala Ala Leu Glu Gly His Thr Ala Pro Ser Leu
50 55 60

Val Asp Ala Leu Leu Asp Gln Val Glu Arg Phe Arg Glu Gln Leu Arg
65 70 75 80

Arg Gln Glu Glu Gly Ala Ser Glu Thr Gln Leu Arg Gln Glu Val Glu
85 90 95

Arg Leu Thr Glu Arg Leu Glu Glu Lys Glu Arg Glu Met Gln Gln Leu
100 105 110

Met Ser Gln Pro Gln His Glu Gln Glu Lys Glu Val Val Leu Leu Arg
115 120 125

Arg Ser Val Ala Glu Lys Glu Lys Ala Arg Ala Ala Ser Asp Val Leu
130 135 140

Cys Arg Ser Leu Ala Asp Glu Thr His Gln Leu Arg Arg Thr Leu Ala
145 150 155 160

Ala Thr Ala His Met Cys Gln His Leu Ala Lys Cys Leu Asp Glu Arg
165 170 175

Gln Cys Ala Gln Gly Asp Ala Gly Glu Lys Ser Pro Ala Glu Leu Glu
180 185 190

Gln Thr Ser Ser Asp Ala Ser Gly Gln Ser Val Ile Lys Lys Leu Gln
195 200 205

Glu Glu Asn Arg Leu Leu Lys Gln Lys Val Thr His Val Glu Asp Leu
210 215 220

Asn Ala Lys Trp Gln Arg Tyr Asp Ala Ser Arg Asp Glu Tyr Val Lys
225 230 235 240

Gly Leu His Ala Gln Leu Lys Arg Arg Gln Val Pro Leu Glu Pro Glu
245 250 255

Leu Met Lys Lys Glu Ile Ser Arg Leu Asn Arg Gln Leu Glu Glu Lys
260 265 270

Ile Ser Asp Cys Ala Glu Ala Asn Gln Glu Leu Thr Ala Met Arg Met
275 280 285

Ser Arg Asp Thr Ala Leu Glu Arg Val Gln Met Leu Glu Gln Gln Ile
290 295 300

Leu Ala Tyr Lys Asp Asp Phe Lys Ser Glu Arg Ala Asp Arg Glu Arg
305 310 315 320

Ala His Ser Arg Ile Gln Glu Leu Glu Glu Lys Ile Met Ser Leu Met
325 330 335

Tyr Gln Val Ser Gln Arg Gln Asp Ser Arg Glu Pro Gly Pro Cys Arg
 340 345 350

Ile His Thr Gly Asn Lys Thr Ala Lys Tyr Leu Glu Met Asp Ala Leu
 355 360 365

Glu His Val Thr Pro Gly Gly Trp Arg Pro Glu Ser Arg Ser Gln Gln
 370 375 380

Met Glu Pro Ser Ala Glu Gly Gly His Val Cys Thr Ala Gln Arg Gly
 385 390 395 400

Gln Gly Asp Leu Gln Cys Pro His Cys Leu Arg Cys Phe Ser Asp Glu
 405 410 415

Gln Gly Glu Ala Phe Leu Arg His Leu Ser Glu Cys Cys Gln
 420 425 430

<210> 7

<211> 410

<212> PRT

<213> Mus musculus

<400> 7

Leu Cys Gly Leu Tyr His Glu Ala Gly Gln Gln Leu Gln Arg Leu Lys
 1 5 10 15

Asp Gln Leu Ala Ala Arg Asp Ala Leu Ile Ala Ser Leu Arg Thr Arg
 20 25 30

Leu Ala Ala Leu Glu Gly His Thr Ala Pro Ser Leu Val Asp Ala Leu
35 40 45

Leu Asp Gln Val Glu Arg Phe Arg Glu Gln Leu Arg Arg Gln Glu Glu
50 55 60

Gly Ala Ser Glu Thr Gln Leu Arg Gln Glu Val Glu Arg Leu Thr Glu
65 70 75 80

Arg Leu Glu Glu Lys Glu Arg Glu Met Gln Gln Leu Met Ser Gln Pro
85 90 95

Gln His Glu Gln Glu Lys Glu Val Val Leu Leu Arg Arg Ser Val Ala
100 105 110

Glu Lys Glu Lys Ala Arg Ala Ala Ser Asp Val Leu Cys Arg Ser Leu
115 120 125

Ala Asp Glu Thr His Gln Leu Arg Arg Thr Leu Ala Ala Thr Ala His
130 135 140

Met Cys Gln His Leu Ala Lys Cys Leu Asp Glu Arg Gln Cys Ala Gln
145 150 155 160

Gly Asp Ala Gly Glu Lys Ser Pro Ala Glu Leu Glu Gln Thr Ser Ser
165 170 175

Asp Ala Ser Gly Gln Ser Val Ile Lys Lys Leu Gln Glu Glu Asn Arg
180 185 190

Leu Leu Lys Gln Lys Val Thr His Val Glu Asp Leu Asn Ala Lys Trp
195 200 205

Gln Arg Tyr Asp Ala Ser Arg Asp Glu Tyr Val Lys Gly Leu His Ala
210 215 220

Gln Leu Lys Arg Arg Gln Val Pro Leu Glu Pro Glu Leu Met Lys Lys
225 230 235 240

Glu Ile Ser Arg Leu Asn Arg Gln Leu Glu Glu Lys Ile Ser Asp Cys
245 250 255

Ala Glu Ala Asn Gln Glu Leu Thr Ala Met Arg Met Ser Arg Asp Thr
260 265 270

Ala Leu Glu Arg Val Gln Met Leu Glu Gln Gln Ile Leu Ala Tyr Lys
275 280 285

Asp Asp Phe Lys Ser Glu Arg Ala Asp Arg Glu Arg Ala His Ser Arg
290 295 300

Ile Gln Glu Leu Glu Glu Lys Ile Met Ser Leu Met Tyr Gln Val Ser
305 310 315 320

Gln Arg Gln Asp Ser Arg Glu Pro Gly Pro Cys Arg Ile His Thr Gly
325 330 335

Asn Lys Thr Ala Lys Tyr Leu Glu Met Asp Ala Leu Glu His Val Thr
340 345 350

Pro Gly Gly Trp Arg Pro Glu Ser Arg Ser Gln Gln Met Glu Pro Ser
 355 360 365

Ala Glu Gly Gly His Val Cys Thr Ala Gln Arg Gly Gln Gly Asp Leu
 370 375 380

Gln Cys Pro His Cys Leu Arg Cys Phe Ser Asp Glu Gln Gly Glu Ala
 385 390 395 400

Phe Leu Arg His Leu Ser Glu Cys Cys Gln
 405 410

<210> 8

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus amino acid sequence
 1

<220>

<221> misc_feature

<222> (1)..(19)

<223> Xaa can be any amino acid

<400> 8

Glu Xaa Xaa Xaa Lys Glu Ile Xaa Arg Leu Asn Xaa Xaa Leu Glu Glu
 1 5 10 15

Xaa Xaa Ser

<210> 9
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consensus amino acid sequence
 2

<220>
 <221> misc_feature
 <222> (1)..(21)
 <223> Xaa can be any amino acid

<400> 9

Leu Xaa Gln Gln Xaa Xaa Xaa Xaa Xaa Xaa Asp Phe Xaa Xaa Glu Arg
 1 5 10 15

Xaa Asp Arg Glu Arg
 20

<210> 10
 <211> 228
 <212> PRT
 <213> Mus musculus

<400> 10

Arg Gln Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu Asn Lys Ala
 1 5 10 15

Leu Glu Glu Ala Leu Ser Ile Gln Ala Ser Pro Ser Ser Pro Pro Ala
 20 25 30

Ala Phe Gly Ser Pro Glu Gly Val Gly Gly His Leu Arg Lys Gln Glu
 35 40 45

Leu Val Thr Gln Asn Glu Leu Leu Lys Gln Gln Val Lys Ile Phe Glu
 50 55 60

Glu Asp Phe Gln Arg Glu Arg Ser Asp Arg Glu Arg Met Asn Glu Glu
 65 70 75 80

Lys Glu Glu Leu Lys Lys Gln Val Glu Lys Leu Gln Ala Gln Val Thr
 85 90 95

Leu Thr Asn Ala Gln Leu Lys Thr Leu Lys Glu Glu Glu Lys Ala Lys
 100 105 110

Glu Ala Leu Lys Gln Gln Lys Arg Lys Ala Lys Ala Ser Gly Glu Arg
 115 120 125

Tyr His Met Glu Pro His Pro Glu His Val Cys Gly Ala Tyr Pro Tyr
 130 135 140

Ala Tyr Pro Pro Met Pro Ala Met Val Pro His His Ala Tyr Lys Asp
 145 150 155 160

Trp Ser Gln Ile Arg Tyr Pro Pro Pro Pro Val Pro Met Glu His Pro
 165 170 175

Pro Pro His Pro Asn Ser Arg Leu Phe His Leu Pro Glu Tyr Thr Trp
 180 185 190

Arg Pro Pro Cys Ala Gly Ile Arg Asn Gln Ser Ser Gln Val Met Asp
 195 200 205

Pro Pro Pro Asp Arg Pro Ala Glu Pro Glu Ser Ala Asp Asn Asp Cys
 210 215 220

Asp Gly Pro Gln
 225

<210> 11
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 11
 gaataaccagg aggcgcagat ccagcggctc aataaaagctt tggaggaggc

50

<210> 12
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 12
 gttgctgaaa gaggacgtca aaatctttga agagg

35

<210> 13
 <211> 39

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
gcaggtaaaa atctttgaag agaatgccca gaggggaacg

39

<210> 14
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
gcaggtaaaa atctttgaag aggacttcca gaggggaacgg agtgatgcgc aacgcatgcc

60

cg

62

<210> 15
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: mutant ABIN-MUT1

<400> 15

Glu Tyr Gln Glu Ala Gln Ile Gln Arg Leu Asn Lys Ala Leu Glu Glu
1 5 10 15

Ala Leu Ser

<210> 16
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutant ABIN-MUT2

<400> 16

Leu Lys Glu Glu Val Lys Ile Phe Glu Glu Asp Phe Gln Arg Glu Arg
1 5 10 15

Ser Asp Arg Glu Arg
20

<210> 17
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutant ABIN-MUT3

<400> 17

Leu Lys Gln Gln Val Lys Ile Phe Glu Glu Asn Ala Gln Arg Glu Arg
1 5 10 15

Ser Asp Arg Glu Arg
20

<210> 18
<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutant ABIN-MUT4

<400> 18

Leu Lys Gln Gln Val Lys Ile Phe Glu Glu Asp Phe Gln Arg Glu Arg
1 5 10 15

Ser Asp Ala Gln Arg
20

<210> 19

<211> 594

<212> PRT

<213> Mus musculus

<400> 19

Met Glu Ala Ser Arg Leu Arg Gln Lys Ala Glu Glu Leu Val Lys Asp
1 5 10 15

Ser Glu Leu Ser Pro Pro Thr Ser Ala Pro Ser Leu Val Ser Phe Asp
20 25 30

Asp Leu Ala Glu Leu Thr Gly Gln Asp Thr Lys Val Gln Val His Pro
35 40 45

Ala Thr Ser Thr Ala Ala Thr Thr Thr Ala Thr Ala Thr Thr Gly Asn
50 55 60

Ser Met Glu Lys Pro Glu Pro Ala Ser Lys Ser Pro Ser Asn Gly Ala

65

70

75

80

Ser Ser Asp Phe Glu Val Val Pro Thr Glu Glu Gln Asn Ser Pro Glu
 85 90 95

Thr Gly Ser His Pro Thr Asn Met Met Asp Leu Gly Pro Pro Pro Pro
 100 105 110

Glu Asp Ser Asn Leu Lys Leu His Leu Gln Arg Leu Glu Thr Thr Leu
 115 120 125

Ser Val Cys Ala Glu Glu Pro Asp His Ser Gln Leu Phe Thr His Leu
 130 135 140

Gly Arg Met Ala Leu Glu Phe Asn Arg Leu Ala Ser Lys Val His Lys
 145 150 155 160

Asn Glu Gln Arg Thr Ser Ile Leu Gln Thr Leu Cys Glu Gln Leu Arg
 165 170 175

Gln Glu Asn Glu Ala Leu Lys Ala Lys Leu Asp Lys Gly Leu Glu Gln
 180 185 190

Arg Asp Leu Ala Ala Glu Arg Leu Arg Glu Glu Asn Thr Glu Leu Lys
 195 200 205

Lys Leu Leu Met Asn Ser Ser Cys Lys Glu Gly Leu Cys Gly Gln Pro
 210 215 220

Ser Ser Pro Lys Pro Glu Gly Ala Gly Lys Lys Gly Val Ala Gly Gln

225	230	235	240
Gln Gln Ala Ser Val Met Ala Ser Lys Val Pro Glu Ala Gly Ala Phe			
245	250	255	
Gly Ala Ala Glu Lys Lys Val Lys Leu Leu Glu Gln Gln Arg Met Glu			
260	265	270	
Leu Leu Glu Val Asn Lys Gln Trp Asp Gln His Phe Arg Ser Met Lys			
275	280	285	
Gln Gln Tyr Glu Gln Lys Ile Thr Glu Leu Arg Gln Lys Leu Val Asp			
290	295	300	
Leu Gln Lys Gln Val Thr Glu Leu Glu Ala Glu Arg Glu Gln Lys Gln			
305	310	315	320
Arg Asp Phe Asp Arg Lys Leu Leu Leu Ala Lys Ser Lys Ile Glu Met			
325	330	335	
Glu Glu Thr Asp Lys Glu Gln Leu Thr Ala Glu Ala Lys Glu Leu Arg			
340	345	350	
Gln Lys Val Arg Tyr Leu Gln Asp Gln Leu Ser Pro Leu Thr Arg Gln			
355	360	365	
Arg Glu Tyr Gln Glu Lys Glu Ile Gln Arg Leu Asn Lys Ala Leu Glu			
370	375	380	
Glu Ala Leu Ser Ile Gln Ala Ser Pro Ser Ser Pro Pro Ala Ala Phe			

385

390

395

400

Gly Ser Pro Glu Gly Val Gly Gly His Leu Arg Lys Gln Glu Leu Val
 405 410 415

Thr Gln Asn Glu Leu Leu Lys Gln Gln Val Lys Ile Phe Glu Glu Asp
 420 425 430

Phe Gln Arg Glu Arg Ser Asp Arg Glu Arg Met Asn Glu Glu Lys Glu
 435 440 445

Glu Leu Lys Lys Gln Val Glu Lys Leu Gln Ala Gln Val Thr Leu Thr
 450 455 460

Asn Ala Gln Leu Lys Thr Leu Lys Glu Glu Glu Lys Ala Lys Glu Ala
 465 470 475 480

Leu Lys Gln Gln Lys Arg Lys Ala Lys Ala Ser Gly Glu Arg Tyr His
 485 490 495

Met Glu Pro His Pro Glu His Val Cys Gly Ala Tyr Pro Tyr Ala Tyr
 500 505 510

Pro Pro Met Pro Ala Met Val Pro His His Ala Tyr Lys Asp Trp Ser
 515 520 525

Gln Ile Arg Tyr Pro Pro Pro Pro Val Pro Met Glu His Pro Pro Pro
 530 535 540

His Pro Asn Ser Arg Leu Phe His Leu Pro Glu Tyr Thr Trp Arg Pro

545

550

555

560

Pro Cys Ala Gly Ile Arg Asn Gln Ser Ser Gln Val Met Asp Pro Pro

565

570

575

Pro Asp Arg Pro Ala Glu Pro Glu Ser Ala Asp Asn Asp Cys Asp Gly

580

585

590

Pro Gln